

FIGURE 1A

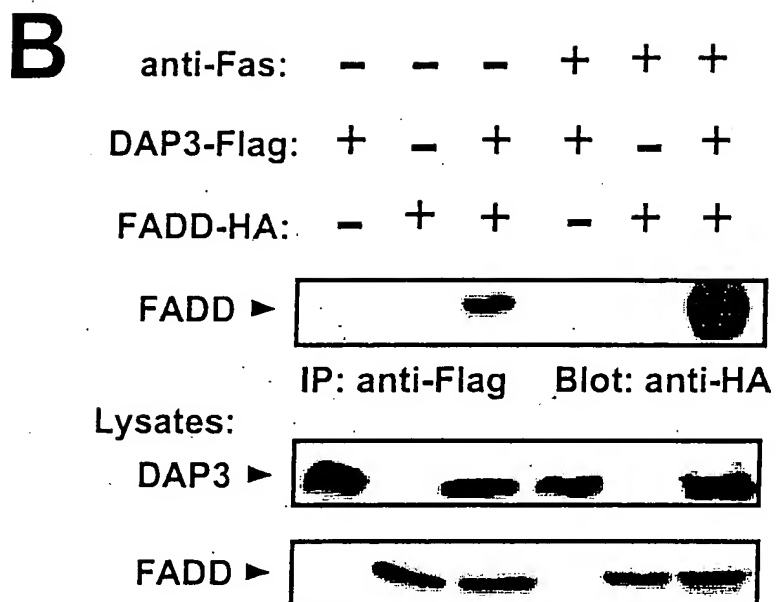


FIGURE 1B

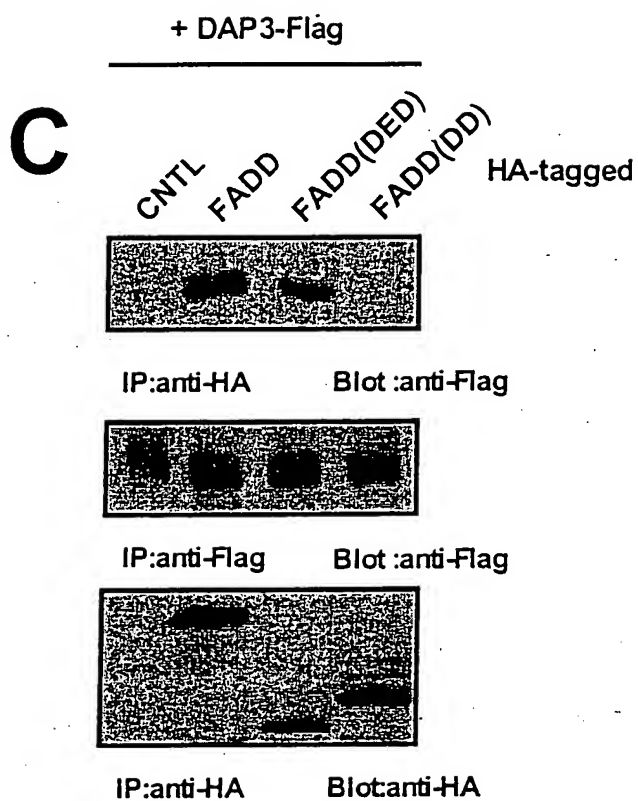


FIGURE 1C

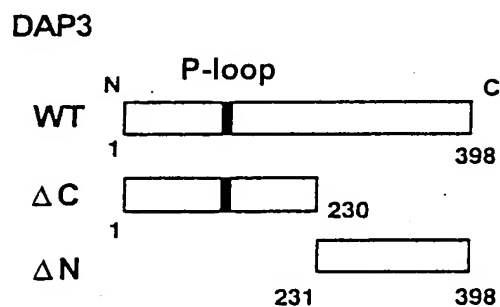
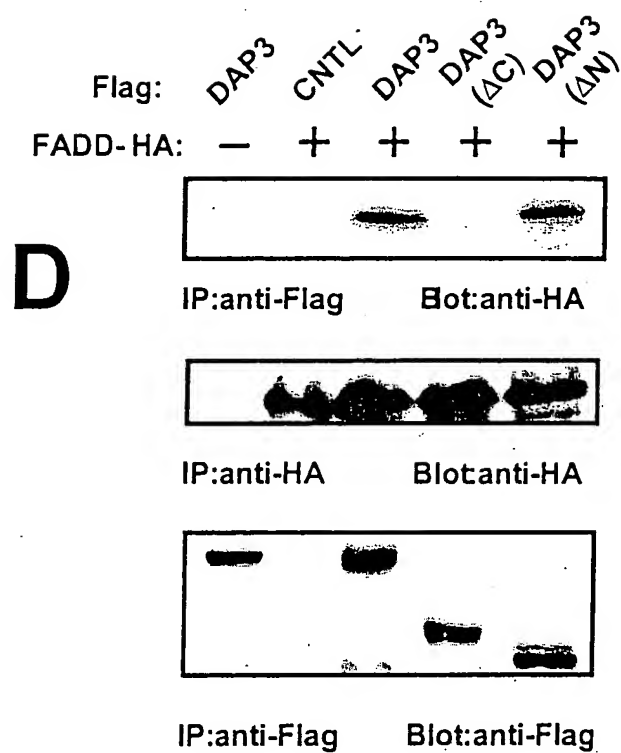


FIGURE 1D

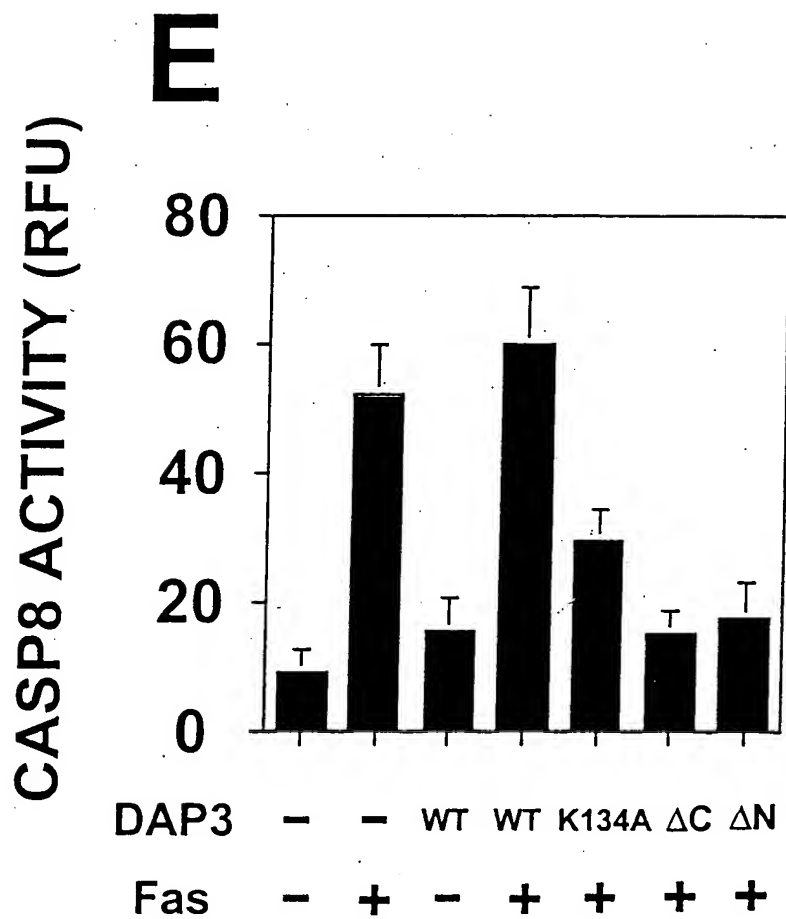


FIGURE 1E

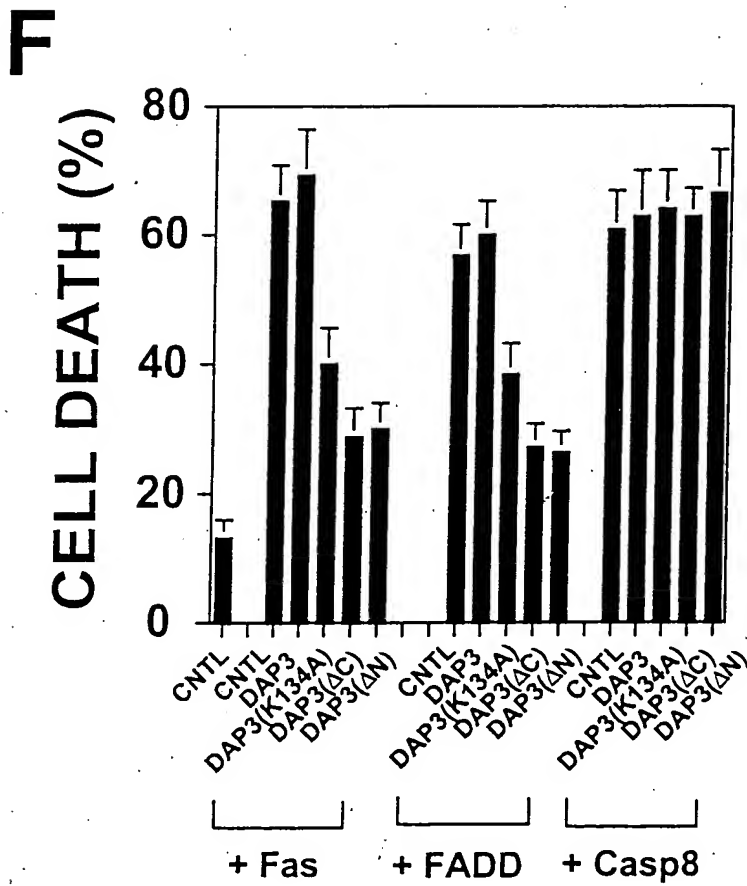


FIGURE 1F

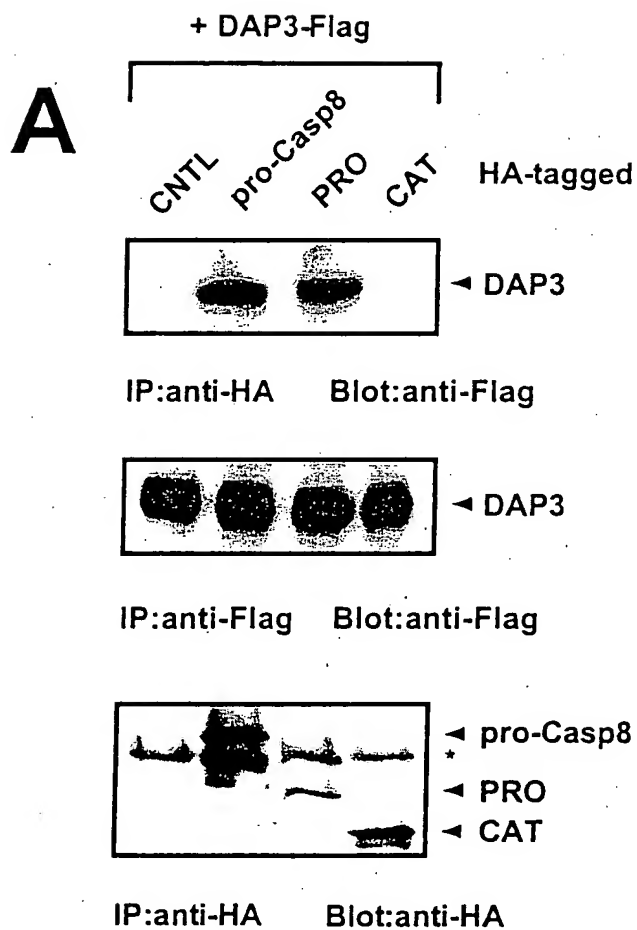


FIGURE 2A

B

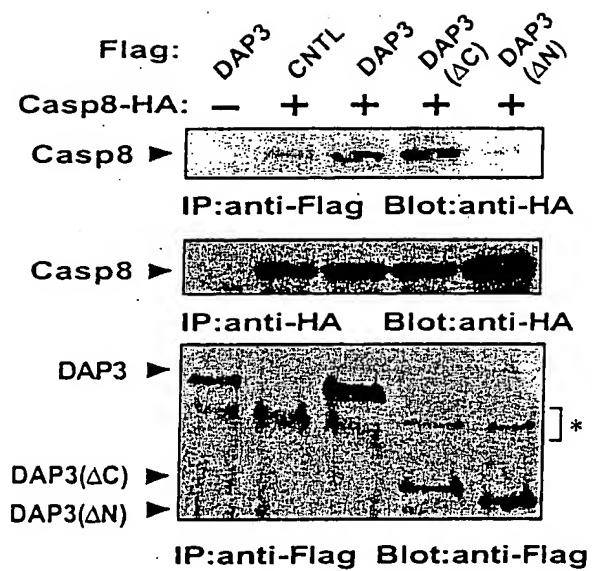


FIGURE 2B

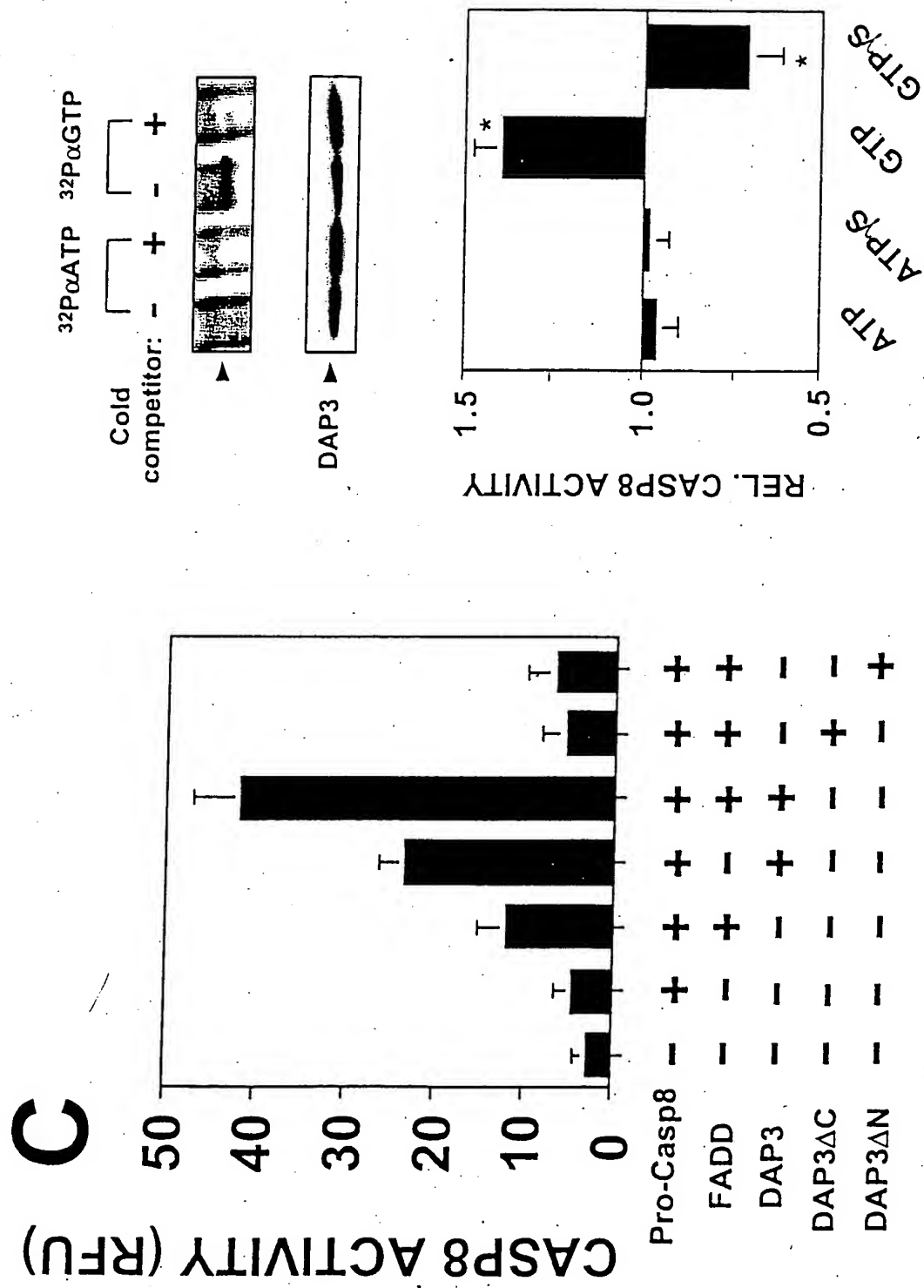


FIGURE 2C

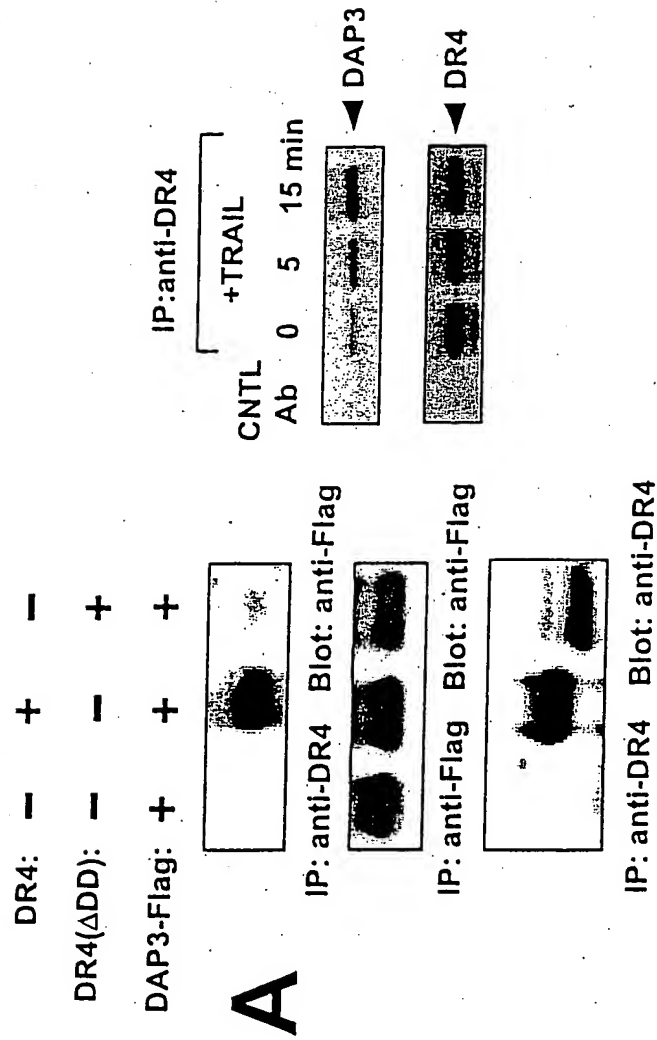


FIGURE 3A



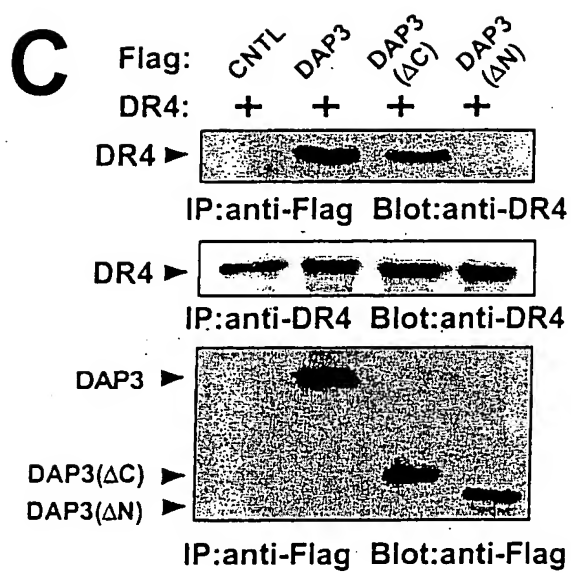
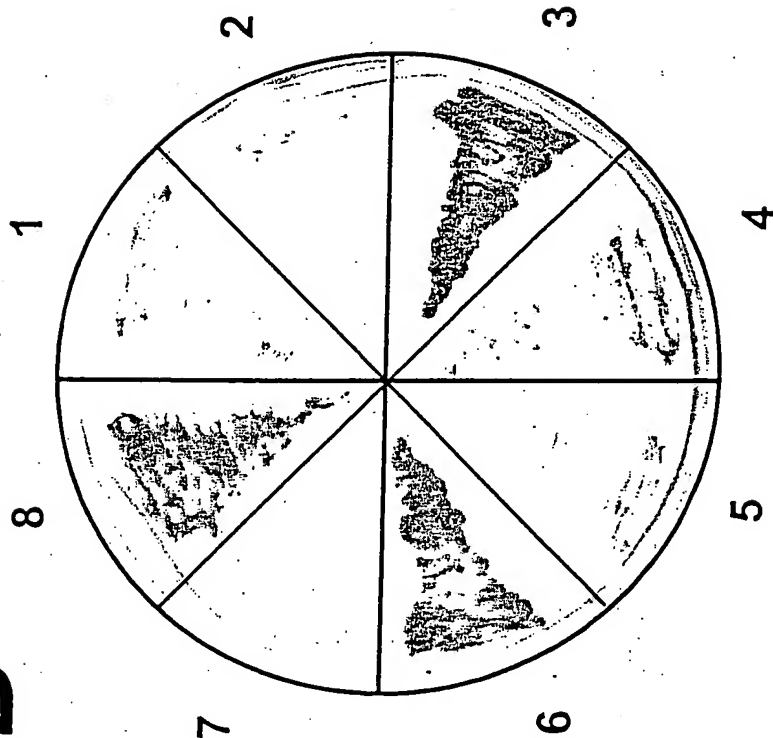


FIGURE 3C

D



DBD TA DAP3 Result

1: DR4	-	-	-
2: DR4	FADD	-	-
3: DR4	FADD	+	+
4: DR5	-	-	-
5: DR5	FADD	-	-
6: DR5	FADD	+	+
7: Fas	-	-	-
8: Fas	FADD	-	+

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FIGURE 3D

E

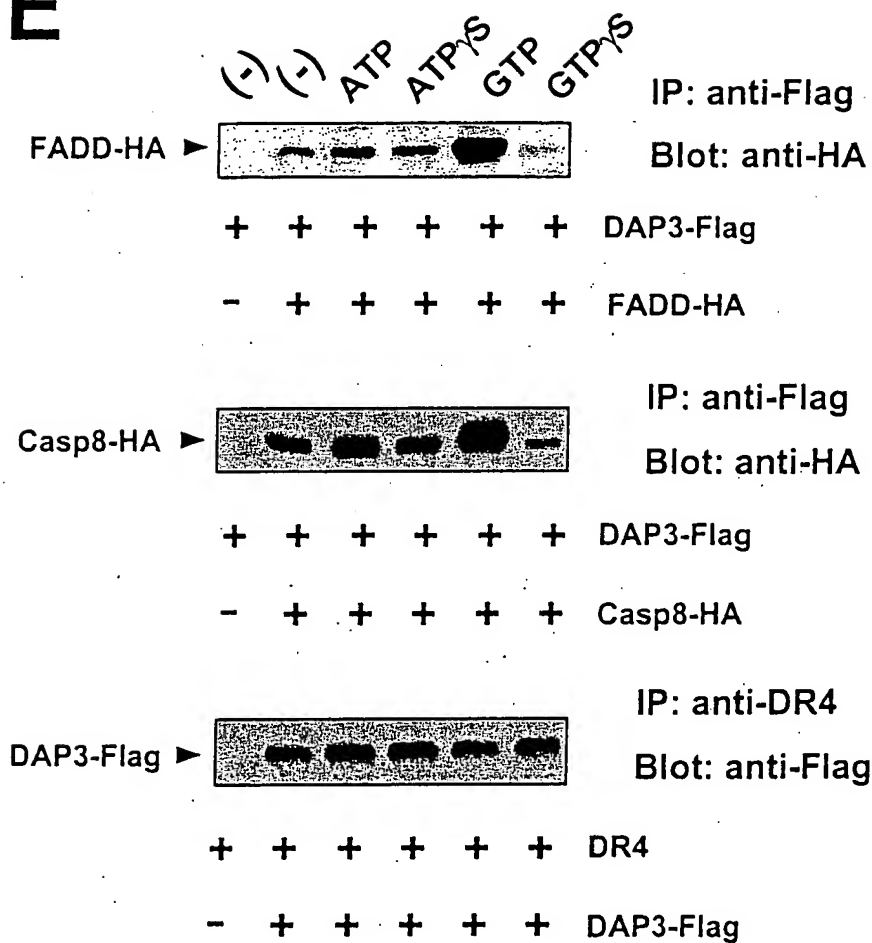


FIGURE 3E

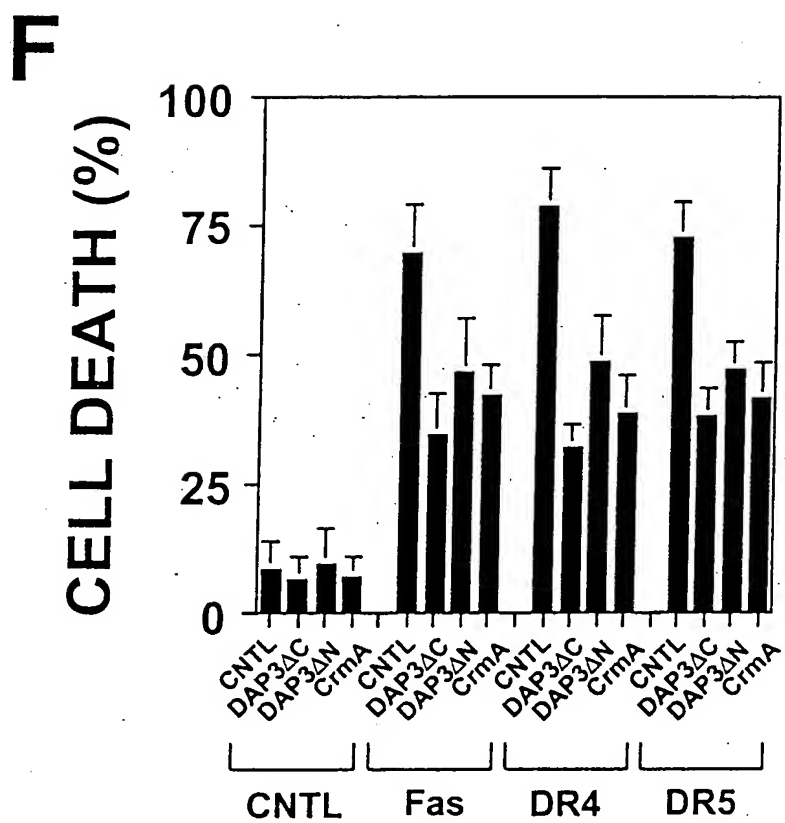


FIGURE 3F

DAP3
agtcctcga ctcacgtgca aggatgatgc tgaaaggaata
_____ antisense 1
_____ antisense 2
_____ antisense 3

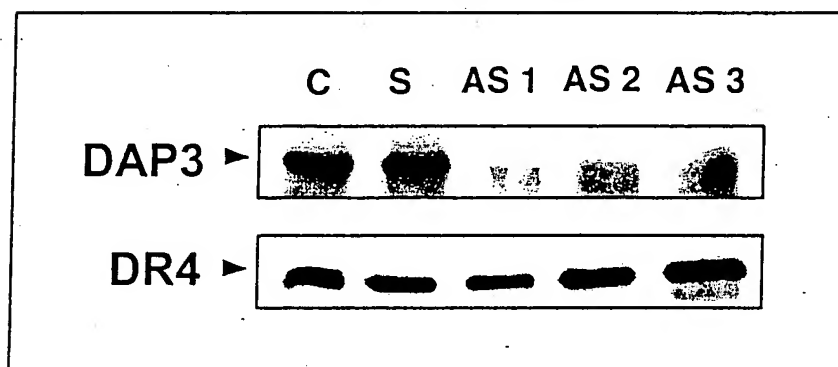
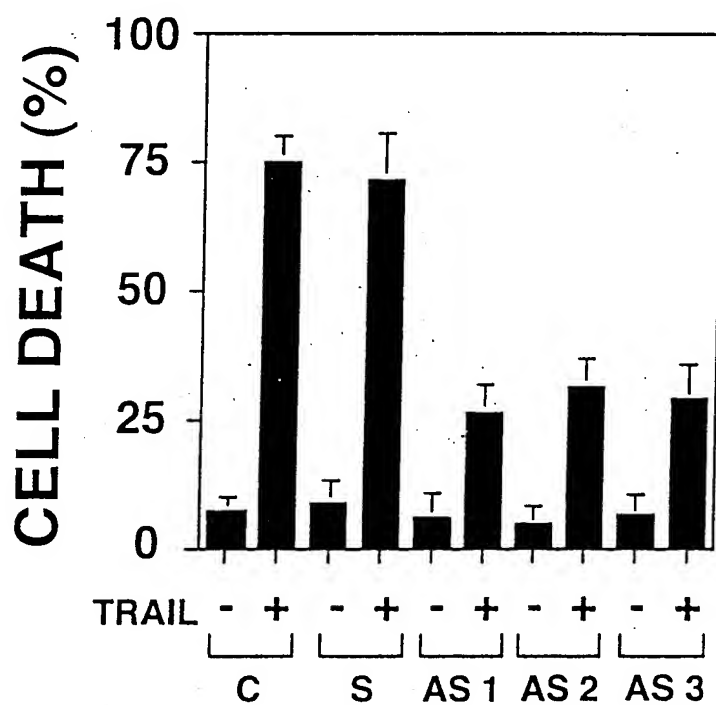


FIGURE 3G

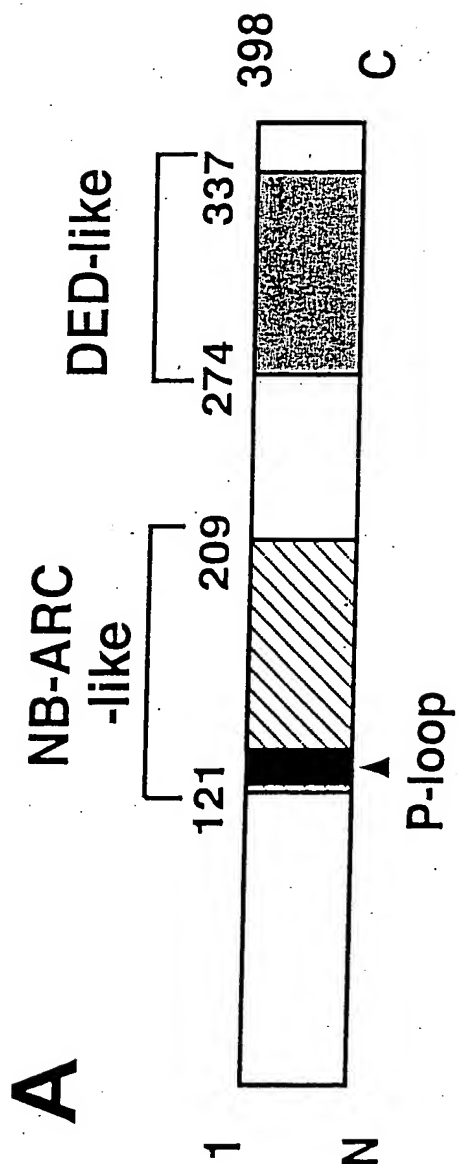


FIGURE 4A

B

115 T S F A Y P A I R Y L L G E K G I G K I S L C H V P H F C A K Q D W L S V G K Q DAP3
 142 K G - E P G W V T T H G M A G C G K S V A A E A A S Q A L E G C F P G G V H W W S V G K Q Apaf1N
 146 E M C D L D S F L L H G C A G S G K S V A A S Q A L E G C F P G G V H W W S V G K Q CED4

152 - - - - - * * * * *
 191 D K S G L L M K L Q I C T R L D Q D L S F S Q R L P L N E E A K D R L R L W V K N C R D L A Q S S Y DAP3
 196 A P K S T F D L F T D L L M L K S E D D L - L N F P S V E H V T S V V L R L W V K N C R D L A Q S S Y Apaf1N
 174 N K Q R F D Q P L E A S T - - - - - L K N F K - - - - - T T N E R F E N Q I K V Q E K Y V W N K R DAP3
 238 S L L L D D V W D S - - - - - W V L K A F D S C Q I L L T T R D V E S N A A S Q T C E F V E Apaf1N
 245 T L F V F D D V W D E T I R W A - C E L R L R C - - - - - L V T T R D V E S N A A S Q T C E F V E CED4

C

268 L W G R T L L K R E D N S P Q E E E L A L V H N L - - - - - R K M K N D W H G G A V S A L S DAP3 DED
 1 M D L F S R N L Y D I I S E E L A S L K F L S L D Y L P Q R K Q E P I K D A L M L F Q R L Q Casp8 DED1
 98 H L L I R V K L L Y I I S E E L A S L K F L S L D Y L P Q R K Q E P I K D A L M L F Q R L Q Casp8 DED2
 17 K V S F R E K L L I I D S N L G V D V E N L K F L C I G L V P K K L E K S S A S D V F E H L L E Casp10 DED1
 121 V S L F R N L L Y E S E S S L S S S E L L K D M I L F L K D S V P K T E M T S - - - L S F L A F L E Casp10 DED2
 1 MD P F L V L L H S V S S L S S S E L L K D M I L F L K D S V P K T E M T S - - - L S F L A F L E FADD DED

312 Q T G S L F K P R K A L P Q E L L G K E G F D A L L
 50 E K R M L E E S N L S F L K E L L F R I N R L D L L
 148 K R V I L G E G K L D I L K R C A Q I N K - S L L L Q
 67 A E D L L S E E D P F L A E L L Y I I R Q K - K L L R
 167 K Q G K L L E E N L C L E D L C K T V R H D L L R
 51 E Q N D L E P G H T E L L R E L L A S L R R H D L L R

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FIGURE 4B, C

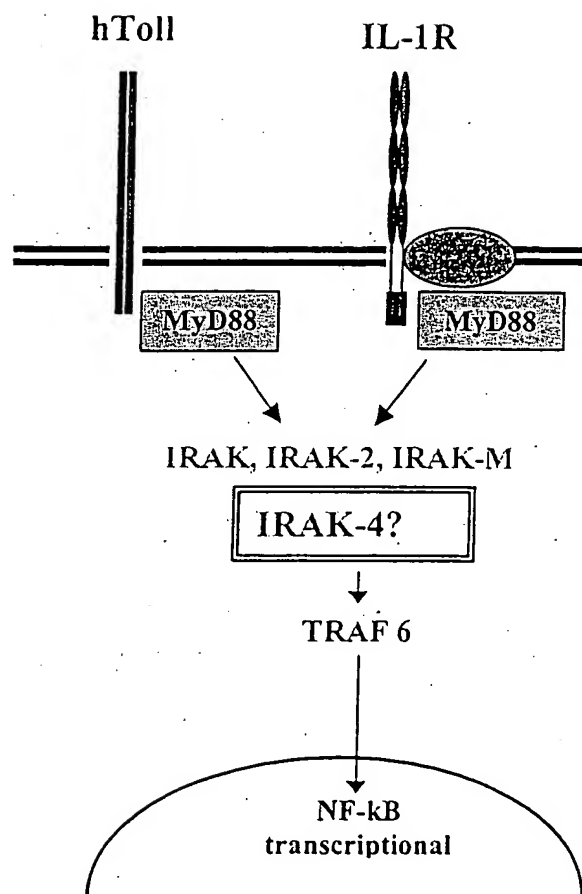


FIGURE 5

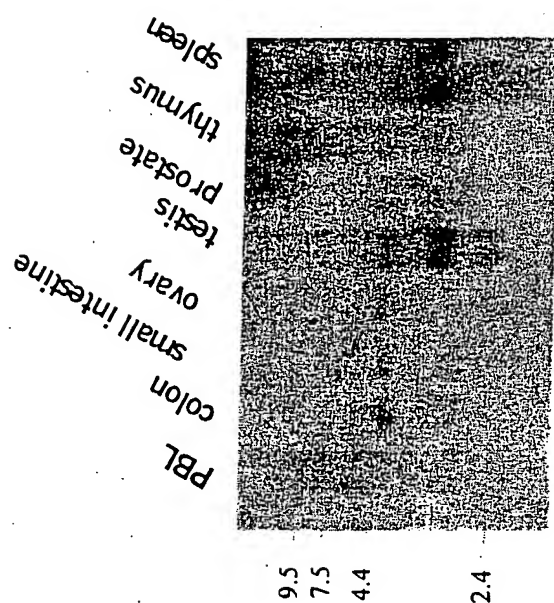


FIGURE 6

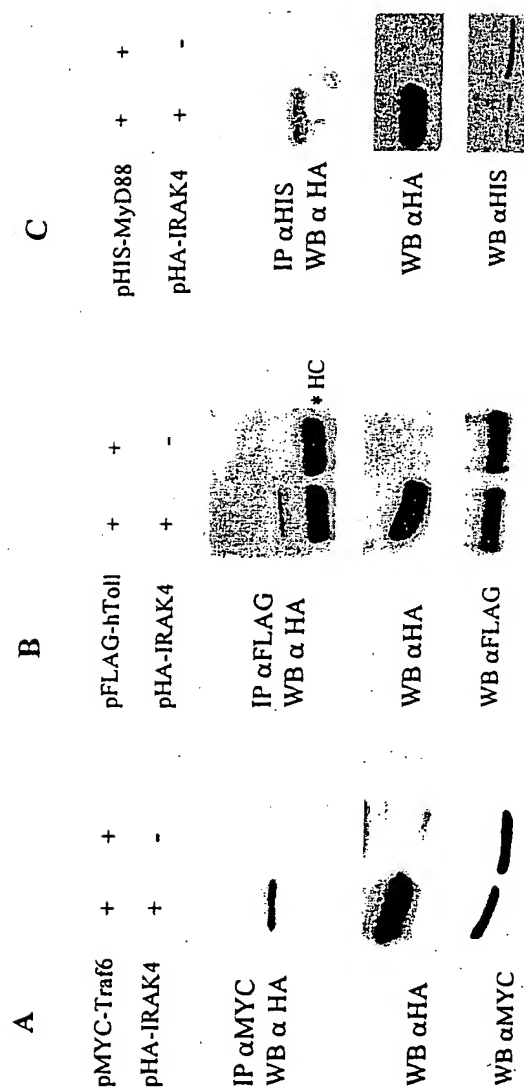


FIGURE 7

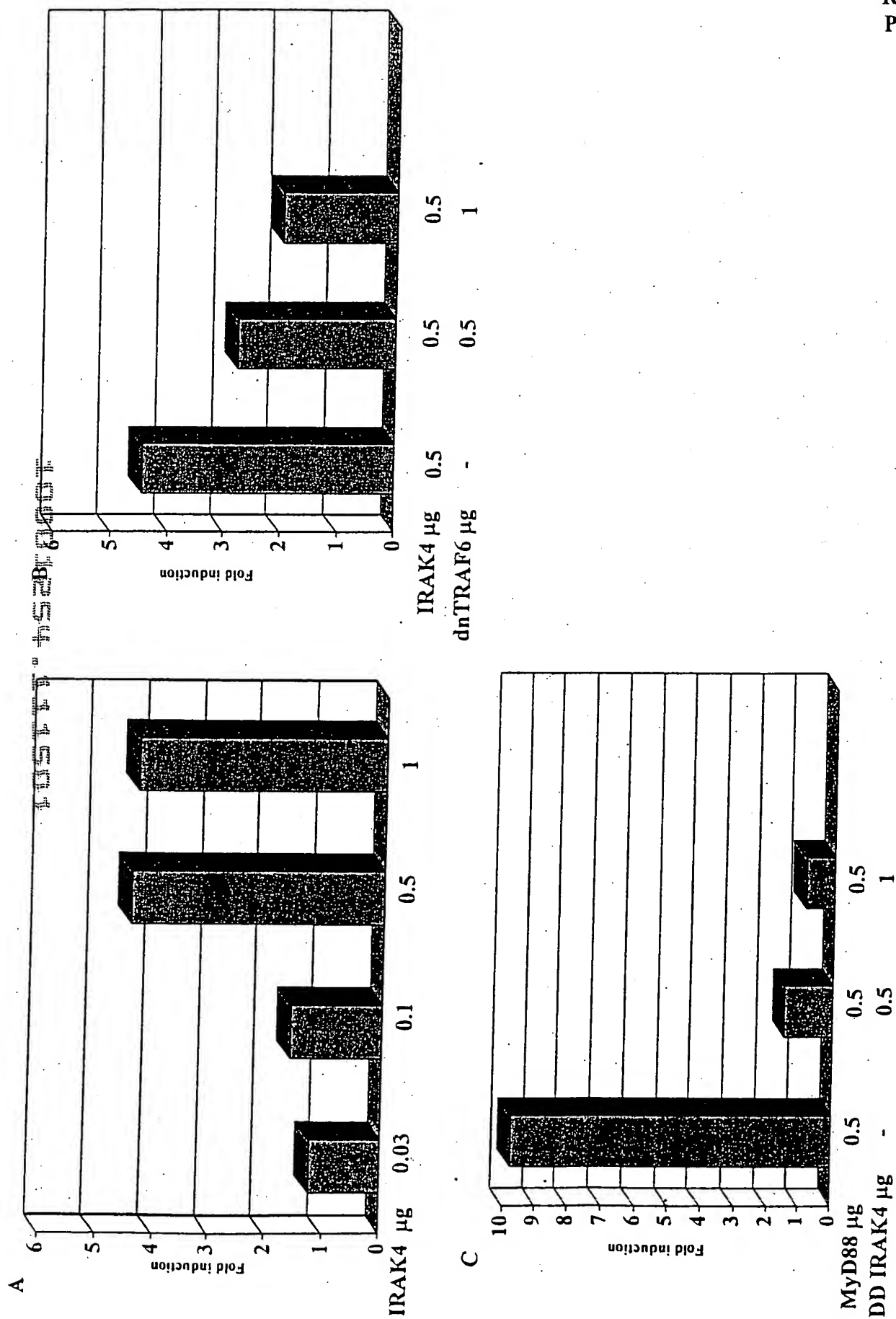


FIGURE 8

DED_4
4758144_hDEDD
6755835_mDEDD
7673638_fDedd1
PDB_FADD_1A1Z

```

WEEDCELDYGMSSHHMREVA GGOTTECEETTAARHDEA-----PG
PPEHGEQEHGASHHMREVGTHETHDVSSTHWDYDE-----D
PPEHGEQEHGASHHMREVGTHETHDVSSTHWDYDE-----D
NEETECSSHEETSHHEEHEVGSOTETCGGEVAHDEETPGHPEDPEGTEDPPG
MPPEHSHSVSSSSSSSEETEMTCG-----MG

```

DED_4
4758144_hDEDD
6755835_mDEDD
7673638_fDedd1
PDB_FADD_1A1Z

```

AAGG-----EA--ASGELEEEEGQCESNTH
HEHG-----ENGDAEAEGCESNTH
HEHG-----ENGDAEAEGCESNTH
PEGSPQANTPCPSSNO MQPQEGCSHASHPSGELEEEEGMSSEANLPE
-----ESVOSGDELSSTHEONDEPGHTE

```

DED_4
4758144_hDEDD
6755835_mDEDD
7673638_fDedd1
PDB_FADD_1A1Z

```

GQELVLAHDSPHLA PPS
QELVLAHDSPTAACP
QELVLAHDSPTAACP
QELVLAHDSPTAACP
QELVLAHDSPTAACP
ELLASHDSPTAACP

```

FIGURE 9

10004452000

a tgaacaaacc cataacacca tcaacatatg tgcgctgcct caatggttga ctaattagga agctgtcaga
 ttttattgat cctcaagaag gatggaagaa gttagctgta gctattaaaa aaccatctgg
 tgatgataga tacaatcagt ttcacataag gagatttgaa gcattacttc aaactggaaa
 aagtcceact tctgaattac tgtttgactg gggcaccaca aattgcacag ttggtgatct
 tgtggatctt ttgatccaaa atgaattttt tgctcctgcg agtcttttgc tcccagatgc
 tgttcccaaa actgctaata cactaccttc taaagaagct ataacagttc agcaaaaaca
 gatgcctttc tgtgacaaaag acaggacatt gatgacacct gtgcagaatc ttgaacaaag
 ctatatgcca cctgactcct caagtccaga aaataaaaagt ttagaagtta gtgatacacg
 ttttcacagt ttttcatttt atgaattgaa gaatgtcaca aataactttg atgaacgacc
 catttctggt ggtggtaata aaatgggaga gggaggattt ggagttgtat ataaaggcta
 cgtaaaatac acaactgtgg cagtgaagaa gcttgcagca atggttgaca ttactactga
 agaactgaaa cagcagtttg atcaagaaat aaaagtaatg gcaaagtgtc aacatgaaaa
 cttagtagaa ctacttggtt tctcaagtga tggagatgac ctctgcttag tatatgttta
 catgcctaata ggttcattgc tagacagact ctcttgcttg gatggtactc caccacttc
 ttggcacatg agatgcaaga ttgctcaggg tgcagctaata ggcatacaatt ttctacatga
 aaatcatcat attcatagag atattaaaag tgcaaatatc ttactggatg aagcttttac
 tgctaaaata tctgactttg gccttgcacg ggcttctgag aagtttgccc agacagtcac
 gactagcaga attgtgggaa caacagctta tatggcacca gaagctttgc gtggagaaat
 aacacccaaa tctgatattt acagcttttg tgtggtttta ctagaaataa taactggact
 tccagctgtg gatgaacacc gtgaacctca gttattgcta gatattaaag aagaaattga
 agatgaagaa aagacaattg aagatttatat tgataaaaag atgaatgatg ctgattccac
 ttcagttgaa gctatgtact ctgttgctag tcaatgtctg catgaaaaga aaaataagag
 accagacatt aagaagggtc aacagctgct gcaagagatg acagcttctt aa

1001254-11501

FIGURE 10A

MNKPITPSTYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSG
DDRYNQFHIRRFEALLQTGKSPTSELLFDWGTNCTVGDLVDLLIQNEFFAPASLLLP
DAVPKTANTLPSKEAITVQQKQMPFCDKORTLMTPVQNLEQSYMPPDSSSPENKSLEV
SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEFGGVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRISC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEEIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNRDPDIKKV
QQLLQEMTAS

1001254.11501

FIGURE 10B

Death domains:

C. pneumoniae

DLWRQFALSLGVSEELANHEFSQAAQDMVATFRRLCDMPQLAVGLGALYTYEIQIPQVCVEKIR

C. muridarum

DLWKQFVFALGVSSEELAHEPSEAAKAKVATFMRWCTGDSLAAAGVAALYSYESQIPCVAKEKIR

C. psittaci

DLWKNFAYALGVTEEELENHVPSAAAQKKVDTFLRWCTGDSL SAGVAALYTYESQIPTVAETKIS

1003254.11504

FIGURE 11A

GI:7190927

ORGANISM *Chlamydia muridarum*

ORIGIN

1 mesrkgikev smnfldqla iiqnkhmleh pfymkwske ltkeqlqaya
kdyylhikaf

61 pkylsaihsr cddlearkll ldnlmdeeng ypnhidlwq fvfalgvsse
eleahepsea

121 akakvatfmr wctgdslaag vaalysyesq ipcvakekir glieyfgfsn
pedyayfteh

181 eeadvrhare ekaliemlsr ddsdkvleas revtqslygf ldsflepatc
chchka

GI:7468151

ORGANISM *Chlamydophila pneumoniae* [*Chlamydia pneumoniae*]

ORIGIN

1 mtswielldk qiedqhmlkh efyqrwsegk lekqqlqaya kdyylhikaf
pcylsalhar

61 cddlqirrqi lenlmdeeag npnhidlwrq falslgvsee elanhefsqa
aqdmvatfrr

121 lcdmpqlavg lgalytyeiq ipqvcvekir glkeyfgvsa rgyayftvhq
eadikhasee

181 kemlqtlvgr enpdavlggs qevldtlwnf lssfinstep csck

FIGURE 11B

6405 ttaagc tttgtgacaa
6421 tgacaacatg ttgcaggctc taaaaatgaa tccaaaaaagc cgtataaaga ttgtgtaact
6481 tctcgcgaag cttctaaaaac tttgtcgcta tcatctctag acaacatctc aattaaggcc
6541 ttttcttccc tagcatgacg cacatcagct tcttcatgct ccgtgaaata agcataatct
6601 tcaggattag aaaagccaaa gtactcaatc aatccacgaa ttttttcttt agctacgcaa
6661 ggaatttgac tttcataaga atacaaagcc gctactcctg ctgctaaaga atcccctgtg
6721 caccaccgca taaatgtcgc aaccttagct ttagctgctt cactgggttc atgagcttct
6781 agctcttctg aagacactcc aagagcaaac acaaattggt tccataaatc aatatgatta
6841 ggataaccat tctcttcac cattaagtta tctaataata acttgcgggc ttctaaatca
6901 tcacaacggc tatgaatagc agataaatat tttggaaaag ctttgatatg caaatagtaa
6961 tcttttgcgt atgcctgtaa ttgttctttt gtcagctctc cttttgacca cttcatgtaa
7021 aaaggggtgtt ctaacatatg tttgttttga ataattgcat ctagctgac taaaaaatc
7081 atgctcacct cttttattcc ttttcttgat tccac 7115

FIGURE 11C

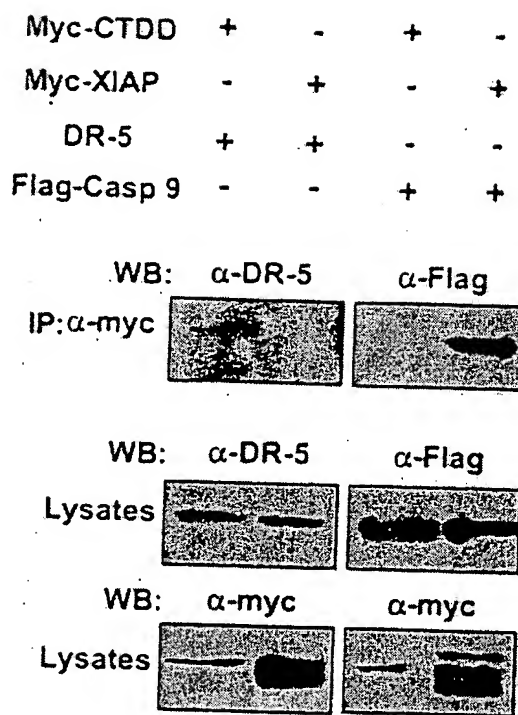


FIGURE 12

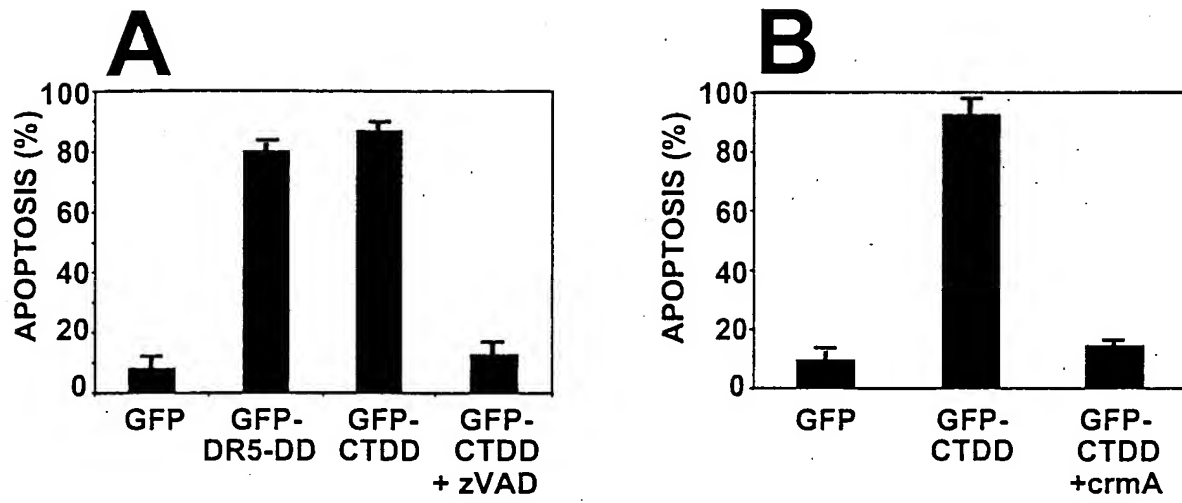


FIGURE 13

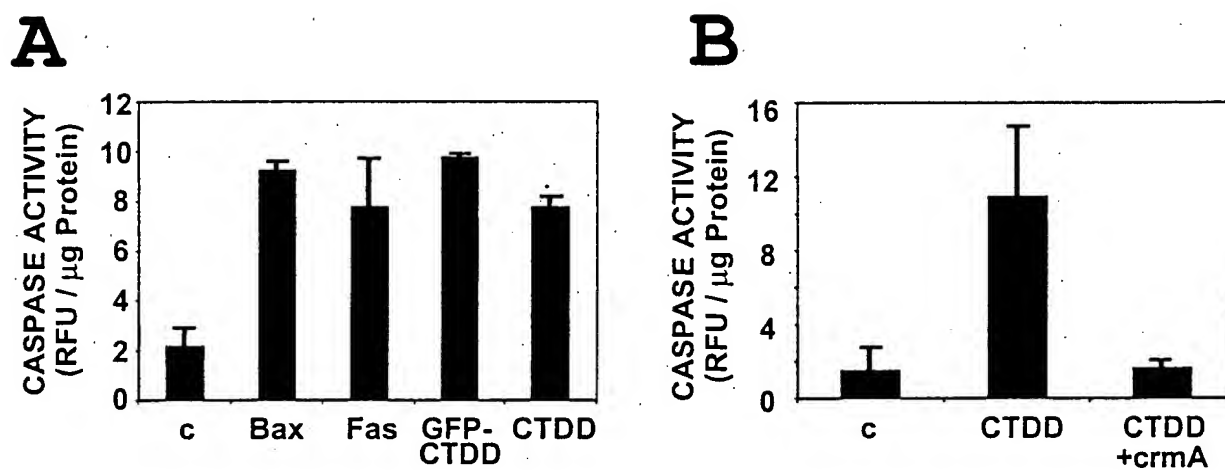


FIGURE 14

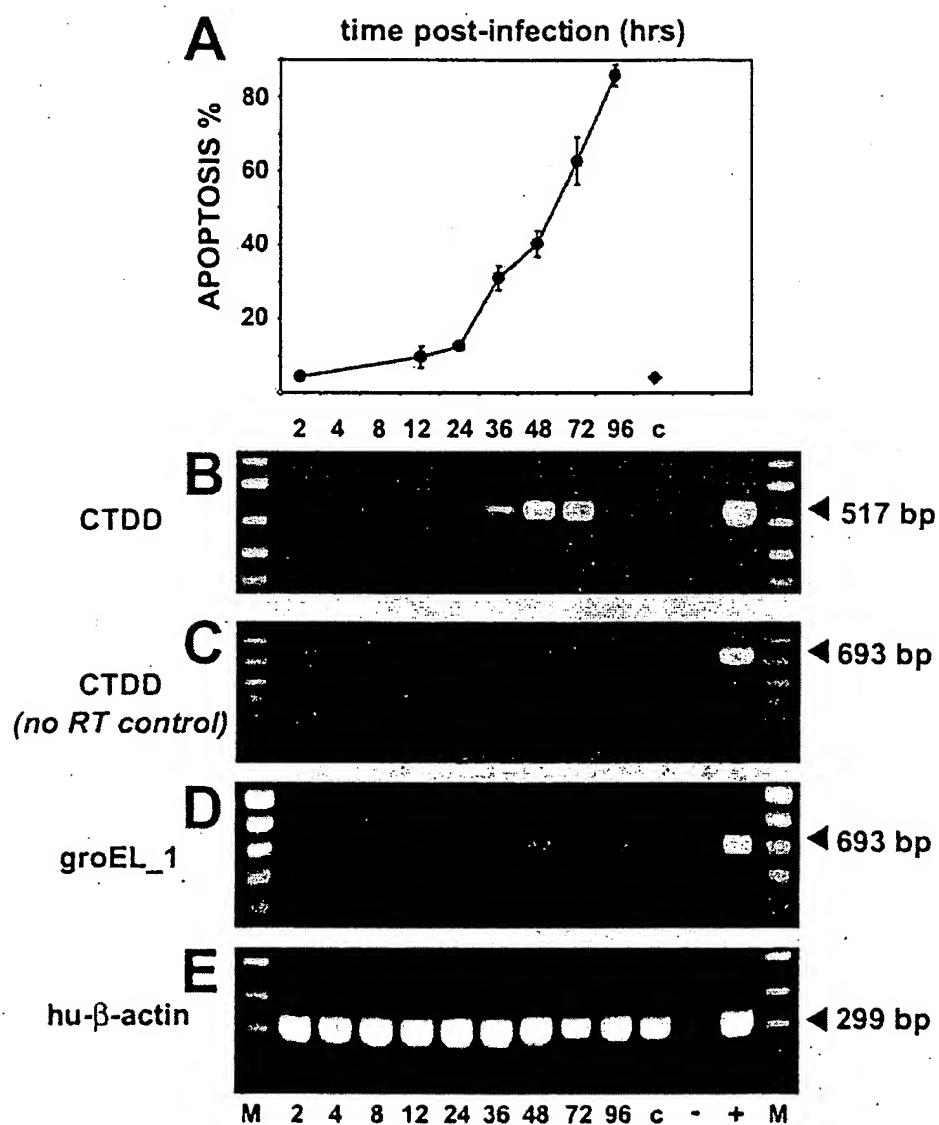


FIGURE 15